RAW SEQUENCE LISTING                    DATE: 12/22/2000
PATENT APPLICATION: US/09/486,167A      TIME: 10:54:34

Input Set : A:\ES.txt
Output Set: N:\CRF3\12222000\I486167A.raw

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 5 <110> APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
 7         UNIVERSITE DE MONS-HAINAUT
11 <120> TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAID PEPTIDE
12         AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG INJURIES AND
13         DISEASES? AND OF OXIDATIVE STRESS-RELATED DISORDERS
17 <130> FILE REFERENCE: VANM143.001A
21 <140> CURRENT APPLICATION NUMBER: US 09/486,167A
23 <141> CURRENT FILING DATE: 2000-08-15
27 <160> NUMBER OF SEQ ID NOS: 4
31 <170> SOFTWARE: PatentIn version 3.0
35 <210> SEQ ID NO: 1
37 <211> LENGTH: 805
39 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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49 <222> LOCATION: (193)..(681)
53 <400> SEQUENCE: 1
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56 ctgagacgct cagcgggcta tatactcgtc ggtggggccg gcggtcagtc tgcggcagcg       120
58 gcagcaagac ggtgcagtga aggagagtgg gcgtctggcg gggtccgcag tttcagcaga       180
60 gccgctgcag cc atg gcc cca atc aag gtg gga gat gcc atc cca gca gtg       231
61            Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala Val
62             1               5                   10
64 gag gtg ttt gaa ggg gag cca ggg aac aag gtg aac ctg gca gag ctg        279
65 Glu Val Phe Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu Leu
66        15                  20                  25
68 ttc aag ggc aag aag ggt gtg ctg ttt gga gtt cct ggg gcc ttc acc        327
69 Phe Lys Gly Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr
70 30                  35                  40                  45
72 cct gga tgt tcc aag aca cac ctg cca ggg ttt gtg gag cag gct gag        375
73 Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu
74             50                  55                  60
76 gct ctg aag gcc aag gga gtc cag gtg gtg gcc tgt ctg agt gtt aat        423
77 Ala Leu Lys Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn
78             65                  70                  75
80 gat gcc ttt gtg act ggc gag tgg ggc cga gcc cac aag gcg gaa ggc        471
81 Asp Ala Phe Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly
82             80                  85                  90
84 aag gtt cgg ctc ctg gct gat ccc act ggg gcc ttt ggg aag gag aca        519
85 Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr
86        95                  100                 105
88 gac tta tta cta gat gat tcg ctg gtg tcc atc ttt ggg aat cga cgt        567
89 Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg
90 110                 115                 120                 125
92 ctc aag agg ttc tcc atg gtg gta cag gat ggc ata gtg aag gcc ctg        615
93 Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu
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94             130              135              140
96 aat gtg gaa cca gat ggc aca ggc ctc acc tgc agc ctg gca ccc aat        663
97 Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn
98             145              150              155
100 atc atc tca cag ctc tga ggccctgggc cagattactt cctccacccc            711
101 Ile Ile Ser Gln Leu
102             160
104 tccctatctc acctgcccag ccctgtgctg gggccctgca attggaatgt tggccagatt     771
106 tctgcaataa acacttgtgg tttgcggaaa aaaa                                805
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111 <211> LENGTH: 162
113 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
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122 1               5                10               15
125 Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu Leu Phe Lys Gly
126             20               25               30
129 Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
130             35               40               45
133 Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu Ala Leu Lys
134       50               55               60
137 Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn Asp Ala Phe
138 65               70               75               80
141 Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly Lys Val Arg
142             85               90               95
145 Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
146             100              105              110
149 Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg Leu Lys Arg
150       115              120              125
153 Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu Asn Val Glu
154       130              135              140
157 Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Ile Ser
158 145             150              155              160
161 Gln Leu
165 <210> SEQ ID NO: 3
167 <211> LENGTH: 780
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179 <222> LOCATION: (136)..(624)
183 <220> FEATURE:
185 <221> NAME/KEY: Unsure
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189 <223> OTHER INFORMATION: purine
193 <220> FEATURE:
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209 <223> OTHER INFORMATION: pyrimidine
213 <400> SEQUENCE: 3
214 tgcgtcctag gcagcatagc cggatcggtg ctccgtgcat cggctacttg gacgtgcgtg      60
216 gcaggcagag caggccggaa aggagcaggt tgggagtgtg gtggggcccg cagcttcagc     120
218 agtgccgcgg tgact atg gcc ccg atc aag gtg gga gac acc att ccc tca      171
219             Met Ala Pro Ile Lys Val Gly Asp Thr Ile Pro Ser
220              1           5                  10
222       gtg gag gta ttt gra ggg gaa cct gga aag aag gtg aac ttg gca gag  219
W--> 223  Val Glu Val Phe Xaa Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu
224          15          20              25
226       ctg ttc aag gac aag aaa ggt gtt ttg ttt gga gtc cct ggg gca ttt  267
227       Leu Phe Lys Asp Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe
228          30          35              40
230       aca cct ggc tgt tcc aag acc cat ctg cct ggg ttt gtg gag caa gcc  315
231       Thr Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala
232       45          50              55              60
234       gga gct cyg aag gcc aag gga gca caa gtg gtg gcc tgt ctg agt gtt  363
W--> 235  Gly Ala Xaa Lys Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val
236          65              70              75
238       aat gat gyc ttc gtg act gca gag tgg ggt cga gcc cac cag gca gaa  411
W--> 239  Asn Asp Xaa Phe Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu
240          80              85              90
242       ggc aag gtt cag ctc ctg gct gac ccc act gga gct ttt gga aag gag  459
243       Gly Lys Val Gln Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu
244          95          100             105
246       aca gat tta cta cta gat gat tct ttg gtg tct ctc ttt ggg aat cgt  507
247       Thr Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg
248          110         115             120
250       cgg cta aaa agg ttc tcc atg gtg ata gac aag ggc gta gta aag gca  555
251       Arg Leu Lys Arg Phe Ser Met Val Ile Asp Lys Gly Val Val Lys Ala
252       125         130             135             140
254       ctg aac gtg gag ccg gat ggc aca ggc ctc acc tgc agc ctg gcc ccc  603
255       Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro
256          145             150             155
258       aac atc ctc tca caa ctc tga ggccctgacc agaatgtcct ctgactctcc     654
259       Asn Ile Leu Ser Gln Leu
260             160
262 catctcctcc acccagctct gggccaaagg cccagtacct ccttacctga gggccactgg     714
264 aatggaacct tgacaatatt tctgcaataa acagtttaat ttgtgaaaaa aaaaaaaaaa     774
266 aaaaaa                                                               780
269 <210> SEQ ID NO: 4
271 <211> LENGTH: 162
273 <212> TYPE: PRT
275 <213> ORGANISM: Rattus rattus
279 <220> FEATURE:
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RAW SEQUENCE LISTING                    DATE: 12/22/2000
PATENT APPLICATION:  US/09/486,167A      TIME: 10:54:34

        Input Set : A:\ES.txt
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     283 <222> LOCATION: 17
     285 <223> OTHER INFORMATION: Glu or Gly
     288 <220> FEATURE:
W--> 290 <221> NAME/KEY: Modified-site
     292 <222> LOCATION: 63
     294 <223> OTHER INFORMATION: Leu or Pro
     297 <220> FEATURE:
W--> 299 <221> NAME/KEY: Modified-site
     301 <222> LOCATION: 79
     303 <223> OTHER INFORMATION: Ala or Val
     306 <400> SEQUENCE: 4
     308 Met Ala Pro Ile Lys Val Gly Asp Thr Ile Pro Ser Val Glu Val Phe
     309 1               5                   10                  15
W--> 312 Xaa Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu Leu Phe Lys Asp
     313             20                  25                  30
     316 Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
     317             35                  40                  45
W--> 320 Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Xaa Lys
     321         50                  55                  60
W--> 324 Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Xaa Phe
     325 65                  70                  75                  80
     328 Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Gln
     329             85                  90                  95
     332 Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
     333             100                 105                 110
     336 Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg Arg Leu Lys Arg
     337             115                 120                 125
     340 Phe Ser Met Val Ile Asp Lys Gly Val Val Lys Ala Leu Asn Val Glu
     341         130                 135                 140
     344 Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Leu Ser
     345 145                 150                 155                 160
     348 Gln Leu
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VERIFICATION SUMMARY                    DATE: 12/22/2000
PATENT APPLICATION:  US/09/486,167A     TIME: 10:54:35

Input Set : A:\ES.txt
Output Set: N:\CRF3\12222000\I486167A.raw

L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
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